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(FILE 'HOME' ENTERED AT 15:07:37 ON 05 APR 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:07:58 ON 05 APR 2006

E BROWN JASON /AU

L1 29 S E3  
E FRANCOIS BERTELLI /AU  
E BERTELLI FRANCOIS /AU

L2 6 S E3

L3 34 S L1 OR L2

L4 2 S L3 AND GABAPENTIN

L5 2 DUP REM L4 (0 DUPLICATES REMOVED)

L6 5760 S GABAPENTIN

L7 134458 S CALCIUM (1W) CHANNEL

L8 430 S L6 (L) L7

L9 13 S GABAPENTIN (1W) BINDING (1W) PROTEIN

L10 7 S L9 (L) L8

L11 5 DUP REM L10 (2 DUPLICATES REMOVED)

L12 7 DUP REM L9 (6 DUPLICATES REMOVED)

L12 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN  
TI Outlooks for a purpose-oriented search for new analgesics: new "targets"  
AU Churyukanov, V. V.; Churyukanov, M. V.  
SO Anesteziologiya i Reanimatologiya (2003), (5), 10-13  
CODEN: AREAD8; ISSN: 0201-7563  
PY 2003  
AB . . . . . kainate and metabotropic receptors, central n-cholinergic  
receptors, vanilloid receptors and purinoceptors, tetrodotoxin-insensitive  
sodium channel SNS/PN3, calcium channels of N-type and **gabapentin**  
**-binding protein**.

L12 ANSWER 2 OF 7 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN  
TI Human alpha2beta2 subunit of calcium channel: a novel **gabapentin**  
**binding protein** in brain.  
AU Su, T. [Reprint author]; Gong, C. H.; Hang, J.; Kohler, W.; Dickerson, M.  
SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract  
No.-40.20. print.  
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New  
Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience.  
ISSN: 0190-5295.  
PY 2000  
TI Human alpha2beta2 subunit of calcium channel: a novel **gabapentin**  
**binding protein** in brain.

L12 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2006 ACS on STN  
TI The race to control pain: more participants, more targets  
AU Chizh, B. A.; Dickenson, A. H.; Wnendt, S.  
SO Trends in Pharmacological Sciences (1999), 20(9), 354-357  
CODEN: TPHSDY; ISSN: 0165-6147  
PY 1999  
AB A review with 49 refs. of some of the recently discovered or re-evaluated  
targets (**gabapentin-binding protein**,  
nicotinic acetylcholine receptors, glutamate receptors, etc.) that have a  
potential for the design of new analgesics.

L12 ANSWER 4 OF 7 MEDLINE on STN DUPLICATE 1  
TI Isolation of the [3H]**gabapentin-binding**  
**protein**/alpha 2 delta Ca2+ channel subunit from porcine brain:  
development of a radioligand binding assay for alpha 2 delta subunits  
using [3H]leucine.  
AU Brown J P; Dissanayake V U; Briggs A R; Milic M R; Gee N S  
SO Analytical biochemistry, (1998 Jan 15) Vol. 255, No. 2, pp. 236-43.  
Journal code: 0370535. ISSN: 0003-2697.  
PY 1998  
TI Isolation of the [3H]**gabapentin-binding**  
**protein**/alpha 2 delta Ca2+ channel subunit from porcine brain:  
development of a radioligand binding assay for alpha 2 delta subunits  
using. . . .

L12 ANSWER 5 OF 7 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN  
TI Structural analysis of calcium channel alpha-2-delta subunit, the  
**gabapentin binding protein**.  
AU Wang, M.; Offord, J.; Oxender, D. L.; Su, T. Z.  
SO FASEB Journal, (1997) Vol. 11, No. 9, pp. A972.  
Meeting Info.: 17th International Congress of Biochemistry and Molecular  
Biology in conjunction with the Annual Meeting of the American Society for  
Biochemistry and Molecular Biology. San Francisco, California, USA. August  
24-29, 1997.  
CODEN: FAJOEC. ISSN: 0892-6638.  
PY 1997  
TI Structural analysis of calcium channel alpha-2-delta subunit, the  
**gabapentin binding protein**.  
IT Miscellaneous Descriptors  
ANALYTICAL METHOD; BIOCHEMISTRY AND BIOPHYSICS; CALCIUM CHANNEL  
ALPHA-2-DELTA SUBUNIT; DISULFIDE LINKAGE FORMATION; **GABAPENTIN**  
**BINDING PROTEIN**; STRUCTURAL ANALYSIS

L12 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 2

TI Spermine modulation of specific [3H]-gabapentin binding to the  
 detergent-solubilized porcine cerebral cortex alpha 2 delta calcium  
 channel subunit.  
 AU Dissanayake V U; Gee N S; Brown J P; Woodruff G N  
 SO British journal of pharmacology, (1997 Mar) Vol. 120, No. 5, pp. 833-40.  
 Journal code: 7502536. ISSN: 0007-1188.  
 PY 1997  
 AB 1. Recent studies have identified the [3H]-**gabapentin-  
 binding protein**, purified from porcine cerebral cortical  
 membranes, as the alpha 2 delta subunit of voltage-sensitive calcium  
 channels (Gee et al., 1996).. . . it was inferred that a second  
 endogenous ligand was removed during dialysis. 5. During initial steps of  
 purification of the [3H]-**gabapentin-binding  
 protein** there was a decrease in the maximum inhibition of  
 [3H]-gabapentin binding by spermine. The loss of the second endogenous  
 molecule. . .

L12 ANSWER 7 OF 7 MEDLINE on STN DUPLICATE 3  
 TI The novel anticonvulsant drug, gabapentin (Neurontin), binds to the  
 alpha2delta subunit of a calcium channel.  
 AU Gee N S; Brown J P; Dissanayake V U; Offord J; Thurlow R; Woodruff G N  
 SO The Journal of biological chemistry, (1996 Mar 8) Vol. 271, No. 10, pp.  
 5768-76.  
 Journal code: 2985121R. ISSN: 0021-9258.  
 PY 1996  
 AB . . . mechanism of action apparently dissimilar to that of other  
 antiepileptic agents. We report here the isolation and characterization  
 of a [3H]**gabapentin-binding protein** from pig  
 cerebral cortex membranes. The detergent-solubilized binding protein was  
 purified 1022-fold, in a six-step column-chromatographic procedure, with a  
 yield. . .

=> d l5 1-2 ti au so py kwic

L5, ANSWER 1 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN  
TI Method for the screening of voltage-dependent calcium channel  
 $\alpha$ 2 $\delta$ -1 subunit binding ligands  
IN Bertelli, Francois; Brown, Jason Peter; Dissanayake, Visaka;  
Suman-Chauhan, Nirmala; Gee, Nicolas Steven  
SO PCT Int. Appl., 157 pp.  
CODEN: PIXXD2  
PY 2001  
2001  
2001  
2002  
2002  
2003  
2003  
2005  
2005  
IN Bertelli, Francois; Brown, Jason Peter; Dissanayake, Visaka;  
Suman-Chauhan, Nirmala; Gee, Nicolas Steven  
IT 327-57-1D, L-Norleucine, labeled derivs. 60142-96-3, Gabapentin  
RL: BOC (Biological occurrence); BSU (Biological study, unclassified);  
BIOL (Biological study); OCCU (Occurrence)  
(-binding site; screening of voltage-dependent calcium channel  
 $\alpha$ 2 $\delta$ -1 subunit-binding ligands)  
IT 61-90-5D, L-Leucine, labeled derivs., biological studies 63-68-3D,  
L-Methionine, labeled derivs., biological studies 63-91-2D,  
L-Phenylalanine, labeled derivs., biological studies 72-18-4D, L-Valine,  
labeled derivs., biological studies 73-32-5D, L-Isoleucine, labeled  
derivs., biological studies 1509-34-8D, L-Allo-isoleucine, labeled  
derivs. 60142-96-3D, Gabapentin, labeled derivs.  
RL: BOC (Biological occurrence); BSU (Biological study, unclassified);  
BIOL (Biological study); OCCU (Occurrence)  
(screening of voltage-dependent calcium channel  $\alpha$ 2 $\delta$ -1  
subunit-binding ligands)  
L5 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2006 ACS on STN  
TI Secreted soluble  $\alpha$ 2 $\delta$ 2,  $\alpha$ 2 $\delta$ 3 or  $\alpha$ 2 $\delta$ 4  
calcium channel subunit polypeptides and screening assays using same  
IN Brown, Jason Peter; Bertelli, Francois  
SO PCT Int. Appl., 160 pp.  
CODEN: PIXXD2  
PY 2001  
2002  
2004  
2001  
2002  
2002  
2003  
2005  
IN Brown, Jason Peter; Bertelli, Francois  
AB . . . screening assays using same. Thus, soluble human  $\alpha$ 2 $\delta$ 2  
and soluble mouse  $\alpha$ 2 $\delta$ 3 subunits were produced in a  
baculovirus-Sf9 cell system. [3H]Gabapentin binding to the  
recombinant human  $\alpha$ 2 $\delta$ 2 subunit was assayed in scintillation  
proximity, Ni flashplate, filter binding, and wheat germ lectin. . .  
IT 61-90-5, L-Leucine, uses 63-68-3, L-Methionine, uses 63-91-2,  
L-Phenylalanine, uses 71-44-3, Spermine 72-18-4, L-Valine, uses  
73-32-5, L-Isoleucine, uses 327-57-1, L-Norleucine 1509-34-8,  
L-Allo-Isoleucine 60142-96-3, Gabapentin  
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)  
(secreted soluble  $\alpha$ 2 $\delta$ 2,  $\alpha$ 2 $\delta$ 3 or  $\alpha$ 2 $\delta$ 4  
calcium channel subunit polypeptides and screening assays using same)

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	7	"6441156"	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:03
L2	7	"6441156" and expression	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:22
L3	0	l2 and gabapectin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:22
L4	5	l2 and gabapentin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:33
L5	5	l1 and gabapentin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:50
L6	45	brown adj jason	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:50
L7	46	brown near jason	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:50
L8	3	bertelli near francois	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:51
L9	46	l7 or l8	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:52
L10	8	l9 and gabapentin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/03/24 08:52

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"6979724"	US-PGPUB; USPAT; DERWENT	OR	ON	2006/04/05 09:33
L2	16	"5846757"	US-PGPUB; USPAT; DERWENT	OR	ON	2006/04/05 11:06
L3	2	"5846757" and gabapentin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/04/05 14:31
L4	1852	"5846757"and gabapentin	US-PGPUB; USPAT; DERWENT	OR	ON	2006/04/05 11:06
L5	2	gabapentin near binding adj protein	US-PGPUB; USPAT; DERWENT	OR	ON	2006/04/05 14:32

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 11, 2006, 00:59:31 ; Search time 53 Seconds  
(without alignments)  
1729.950 Million cell updates/sec

Title: US-10-088-876-6  
Perfect score: 5911  
Sequence: 1 MAVPARTCGASRPGPARTAR.....PHICFDYNATEDTSDCGRGA 1109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	5911	100.0	1109	2	US-09-397-550-6	Sequence 6, Appli
2	5911	100.0	1115	2	US-09-397-550-23	Sequence 23, Appl
3	5911	100.0	1145	2	US-09-470-443-2	Sequence 2, Appli
4	5911	100.0	1145	2	US-09-470-443-4	Sequence 4, Appli
5	5911	100.0	1145	2	US-09-397-550-20	Sequence 20, Appl
6	5753	97.3	1082	2	US-09-397-550-5	Sequence 5, Appli
7	5641	95.4	1062	2	US-09-397-550-4	Sequence 4, Appli
8	5519	93.4	1076	2	US-09-470-443-6	Sequence 6, Appli
9	3025.5	51.2	1063	2	US-10-090-827-8	Sequence 8, Appli
10	3025.5	51.2	1063	2	US-09-397-548-8	Sequence 8, Appli
11	3025.5	51.2	1069	2	US-10-090-827-9	Sequence 9, Appli

12	3025.5	51.2	1091	2	US-10-090-827-5	Sequence 5, Appli
13	3025.5	51.2	1091	2	US-09-397-548-5	Sequence 5, Appli
14	3024	51.2	1084	1	US-08-455-543A-56	Sequence 56, Appl
15	3024	51.2	1084	1	US-08-223-305C-56	Sequence 56, Appl
16	3022	51.1	1106	1	US-08-336-257A-8	Sequence 8, Appli
17	3020	51.1	1106	1	US-08-435-675B-5	Sequence 5, Appli
18	3014.5	51.0	1079	1	US-08-455-543A-55	Sequence 55, Appl
19	3014.5	51.0	1079	1	US-08-223-305C-55	Sequence 55, Appl
20	3011.5	50.9	1103	1	US-08-455-543A-53	Sequence 53, Appl
21	3011.5	50.9	1103	1	US-08-223-305C-53	Sequence 53, Appl
22	3004.5	50.8	1063	2	US-10-090-827-15	Sequence 15, Appl
23	3004.5	50.8	1063	2	US-09-397-548-17	Sequence 17, Appl
24	3004.5	50.8	1091	1	US-07-745-206A-25	Sequence 25, Appl
25	3004.5	50.8	1091	1	US-08-455-543A-52	Sequence 52, Appl
26	3004.5	50.8	1091	1	US-08-223-305C-52	Sequence 52, Appl
27	3004.5	50.8	1091	1	US-08-311-363-25	Sequence 25, Appl
28	3004.5	50.8	1091	2	US-10-162-012-17	Sequence 17, Appl
29	3004.5	50.8	1091	2	US-10-090-827-16	Sequence 16, Appl
30	3004.5	50.8	1091	2	US-09-397-548-14	Sequence 14, Appl
31	3000.5	50.8	1091	2	US-08-713-118-4	Sequence 4, Appli
32	3000.5	50.8	1091	2	US-09-452-007-4	Sequence 4, Appli
33	2995	50.7	1086	1	US-08-455-543A-54	Sequence 54, Appl
34	2995	50.7	1086	1	US-08-223-305C-54	Sequence 54, Appl
35	2924.5	49.5	1036	2	US-10-090-827-7	Sequence 7, Appli
36	2924.5	49.5	1036	2	US-09-397-548-7	Sequence 7, Appli
37	2907.5	49.2	1036	2	US-10-090-827-14	Sequence 14, Appl
38	2907.5	49.2	1036	2	US-09-397-548-16	Sequence 16, Appl
39	2887.5	48.8	1018	2	US-10-090-827-6	Sequence 6, Appli
40	2887.5	48.8	1018	2	US-09-397-548-6	Sequence 6, Appli
41	2872.5	48.6	1018	2	US-10-090-827-13	Sequence 13, Appl
42	2872.5	48.6	1018	2	US-09-397-548-15	Sequence 15, Appl
43	2856	48.3	1086	6	5386025-8	Patent No. 5386025
44	1594.5	27.0	508	1	US-08-435-675B-6	Sequence 6, Appli
45	1186	20.1	1077	2	US-09-397-550-24	Sequence 24, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-397-550-6

; Sequence 6, Application US/09397550

; Patent No. 6783952

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2

; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and

; TITLE OF INVENTION: screening assays using same

; FILE REFERENCE: 180

; CURRENT APPLICATION NUMBER: US/09/397,550

; CURRENT FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 1109

; TYPE: PRT

; ORGANISM: Homo sapiens



US-09-397-550-6

Query Match 100.0%; Score 5911; DB 2; Length 1109;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLLPLLLPLLAAPGAS	60
Db	1	MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLLPLLLPLLAAPGAS	60
Qy	61	AYSFPQQHTMQHWARRLEQEVDGVMRI FGGVQQLREIYKDNRNLFEVQENEPQKLVEKVA	120
Db	61	AYSFPQQHTMQHWARRLEQEVDGVMRI FGGVQQLREIYKDNRNLFEVQENEPQKLVEKVA	120
Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRA PKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRA PKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEEKYNWPNRT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEEKYNWPNRT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIP SIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIP SIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTDGDPGEKKNLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTDGDPGEKKNLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRS MIDGN	600
Db	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRS MIDGN	600
Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSLGLVLPYSTFY LQANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSLGLVLPYSTFY LQANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Qy	721	HNLILDTGITQQ LVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Db	721	HNLILDTGITQQ LVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780

Qy 781 SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRLPAVVGVKLD 840  
 |||  
 Db 781 SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRLPAVVGVKLD 840

Qy 841 LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ 900  
 |||  
 Db 841 LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ 900

Qy 901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960  
 |||  
 Db 901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960

Qy 961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020  
 |||  
 Db 961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020

Qy 1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080  
 |||  
 Db 1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080

Qy 1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109  
 |||  
 Db 1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109

# RESULT 2

US-09-397-550-23

; Sequence 23, Application US/09397550

; Patent No. 6783952

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2

; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and

; TITLE OF INVENTION: screening assays using same

; FILE REFERENCE: 180

; CURRENT APPLICATION NUMBER: US/09/397,550

; CURRENT FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 1115

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-397-550-23

Query Match 100.0%; Score 5911; DB 2; Length 1115;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAVPARTCGASRPGPARTARPWPGCGPHGPGTRRPTSGPPRPLWLLLPLLLPLLAAPGAS 60

|||

Db 1 MAVPARTCGASRPGPARTARPWPGCGPHGPGTRRPTSGPPRPLWLLLPLLLPLLAAPGAS 60

Qy 61 AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQEVQENEPQKLVEKVA 120

|||

Db 61 AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQEVQENEPQKLVEKVA 120

Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSMDGN	600
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Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSLGLVLPYSTFYQLQANLSDQILQV	660
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Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Qy	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Db	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Qy	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Db	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Qy	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900
Db	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900
Qy	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF	960
Db	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF	960



Db	181	GSKASTLRDLFIEDPNFKNVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSMDGN	600
Db	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSMDGN	600
Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPPYSTFYLOANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPPYSTFYLOANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNTEFLKNFIELMEKVT PDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNTEFLKNFIELMEKVT PDSKQCNNFLL	720
Qy	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Db	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Qy	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTL RPAVVGVKLD	840
Db	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTL RPAVVGVKLD	840
Qy	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNE DLLCVLIDDGGFLVLSNQNHQ	900
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Qy	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF	960
Db	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF	960
Qy	961	LNLA WWTSA AAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA	1020
Db	961	LNLA WWTSA AAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA	1020
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RESULT 4
US-09-470-443-4
; Sequence 4, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443-4

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Db	1	MAVPARTCGASRPGPARTARPWPGCGPHGPGTRRPTSGPPRPLWLLLPLLLAAPGAS	60
Qy	61	AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQENEPQKLVEKVA	120
Db	61	AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQENEPQKLVEKVA	120
Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRDLFIEDPNFKNKNVYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRDLFIEDPNFKNKNVYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAOPVSCFTHLVOANVRNKKVFKEAV	360

Db	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFEKYNWPNRT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGKEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGKEA	480
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Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSIDGN	600
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Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPYSTFYQLQANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPYSTFYQLQANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
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Qy	721	HNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
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Qy	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGKLD	840
Db	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGKLD	840
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Db	841	LEAWAEKFKVLASNRTHQDQPKCGPNSHCEMDCEVNEDLLCVLIDDGGFLVLSNQNHQ	900
Qy	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF	960
Db	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF	960
Qy	961	LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAGSPETRESSCVMKQTQYYFGSVNA	1020
Db	961	LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAGSPETRESSCVMKQTQYYFGSVNA	1020
Qy	1021	SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL	1080
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Db	1081	VQRPRYRRGPHICFDYNATEDTSDCGRGA	1109

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 11, 2006, 00:54:50 ; Search time 53 Seconds  
 (without alignments)  
 2013.290 Million cell updates/sec

Title: US-10-088-876-6  
 Perfect score: 5911  
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Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3020	51.1	1106	1	CHRB2	calcium channel pr
2	3004.5	50.8	1091	2	JH0565	calcium channel al
3	2972	50.3	1091	2	A44147	calcium channel pr
4	1186	20.1	1091	2	T30256	calcium channel al
5	558.5	9.4	734	2	S44617	C50C3.11 protein -
6	551	9.3	1148	2	T18770	probable calcium c
7	221	3.7	1450	2	C86880	hypothetical prote
8	175.5	3.0	885	2	S30350	inter-alpha-trypsi
9	169.5	2.9	886	2	S54355	inter-alpha-trypsi
10	164	2.8	436	2	E90261	hypothetical prote
11	163.5	2.8	930	2	JX0368	inter-alpha-trypsi
12	160.5	2.7	709	2	AD2843	methyl-accepting c
13	160.5	2.7	717	2	E97620	methyl-accepting c



14	153.5	2.6	889	2	JC5576	inter-alpha-trypsi
15	151.5	2.6	676	2	T47637	hypothetical prote
16	150.5	2.5	2022	2	T43214	ovt1 protein - nem
17	149	2.5	1132	2	H82887	hypothetical prote
18	148	2.5	418	2	AG2350	hypothetical prote
19	148	2.5	575	2	D64998	hypothetical prote
20	146	2.5	689	2	F84811	probable retroelem
21	144	2.4	796	2	A90541	hypothetical prote
22	140.5	2.4	1957	2	A45627	myosin heavy chain
23	140	2.4	420	2	S76691	hypothetical prote
24	140	2.4	907	2	S54353	inter-alpha-trypsi
25	139.5	2.4	1935	2	T39411	RNA helicase - fis
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27	138	2.3	820	2	AE1886	two-component hybr
28	138	2.3	2401	2	T28676	rhoptry protein -
29	137.5	2.3	911	2	A39967	inter-alpha-trypsi
30	137.5	2.3	2829	2	A42771	reticulocyte-bindi
31	137	2.3	905	2	T02205	Lu-ECAM-1 protein
32	136	2.3	811	2	AB1980	two-component hybr
33	136	2.3	921	2	JC4625	inter-alpha-trypsi
34	136	2.3	1957	2	A59294	skeletal myosin -
35	136	2.3	3343	2	S44887	ZK112.7 protein -
36	135.5	2.3	739	2	H75001	methyl-accepting c
37	134	2.3	1243	2	S60138	sex factor aggrega
38	134	2.3	1256	2	T26101	hypothetical prote
39	133.5	2.3	758	2	C96749	hypothetical prote
40	132.5	2.2	962	2	T01688	starch debranching
41	132	2.2	886	2	D98115	conserved hypothet
42	132	2.2	1144	2	T20218	hypothetical prote
43	130.5	2.2	1471	2	T40117	myosin-2 isoform -
44	130.5	2.2	1516	2	E71619	RAD2 endonuclease
45	129.5	2.2	2089	1	A48757	acetyl-CoA carboxy

#### ALIGNMENTS

##### RESULT 1

##### CHRB2

calcium channel protein alpha-2 chain precursor - rabbit

N;Alternate names: dihydropyridine-binding protein, 140K

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C;Accession: S10579; A39518; A33409

R;Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, K.P.; McKenna, E.; Koch, W.J.; Hui, A.; Schwartz, A.; Harpold, M.M.

Science 241, 1661-1664, 1988

A;Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of a DHP-sensitive calcium channel.

A;Reference number: S10579; MUID:88336904; PMID:2458626

A;Accession: S10579

A;Molecule type: mRNA

A;Residues: 1-1106 <ELL>

A;Cross-references: UNIPROT:P13806; UNIPARC:UPI000012798C; EMBL:M21948;

NID:g164762; PIDN:AAA81562.1; PID:g164763

A;Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found

R;Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.  
 J. Biol. Chem. 266, 3287-3293, 1991  
 A;Title: Structural characterization of the dihydropyridine-sensitive calcium channel alpha-2-subunit and the associated delta peptides.  
 A;Reference number: A39518; MUID:91131638; PMID:1847144  
 A;Accession: A39518  
 A;Molecule type: protein  
 A;Residues: 961-973 <JAY>  
 A;Cross-references: UNIPARC:UPI0000174208  
 A;Note: this sequence represents the amino end of a glycosylated peptide that appears after reduction of disulfide bonds in the mature protein; several forms (25K, 22K, and 17K) have a common sequence at the amino end and identical molecular weights (17K) following deglycosylation  
 R;Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.  
 Biochemistry 28, 7820-7828, 1989  
 A;Title: Subunit composition of the purified dihydropyridine binding protein from skeletal muscle.  
 A;Reference number: A33409; MUID:90122765; PMID:2558713  
 A;Accession: A33409  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 27-44,'S',46-47 <HAM>  
 A;Cross-references: UNIPARC:UPI0000174209  
 C;Superfamily: calcium channel alpha-2 chain  
 C;Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosphoprotein  
 F;1-26/Domain: signal sequence #status predicted <SIG>  
 F;27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>  
 F;94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.1%; Score 3020; DB 1; Length 1106;  
 Best Local Similarity 53.5%; Pred. No. 1.9e-185;  
 Matches 590; Conservative 177; Mismatches 267; Indels 68; Gaps 20;

Qy	42	RPL-----WLLLPLPLLAAPGASAYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQ	92
		:  :      :  :  :  :  :  :	
Db	5	RPLAWTLTLWQAWL-----ILIGP-SSEEPFPSAVTIKSWVDKMQEDLVTLAKTASGVH	57
Qy	93	QLREIYKDNRNLFQVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQD	152
		:  : :  :  :  :            :             :	
Db	58	QLVDIYEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQWRE	117
Qy	153	NIKEEDIVYYDAKADAELDDPESEDVERGSKASTLRDLDFIEDPNFKKNVNSYAAVQIPT	212
		: :   :             : :  :  :  :  :  :	
Db	118	DFASNEVVYYNAKDDL---DPEKNDSEPGSQ--RIKPVFIDDANFRRQVSYQHAHVHIPT	172
Qy	213	DIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW---RAP	268
		:    :          :  :  :  :          :      :	
Db	173	DIYEGSTIVLNELNWTSALEDDVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTP	232
Qy	269	KKIDLYDVRRRPWYIQGASSPKDMVIVDVSGSVSGLTLKLMKTSVCEMLDLSDDDYVN	328
		:      :  :              :          :	
Db	233	NKIDLYDVRRRPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETLSDDDFVN	292
Qy	329	VASFNEKAQPVSCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNIT	388

Db	293	VASFNSNAQDVSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVS	352
Qy	389	RANCNKMIMMFTDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNYDVTPLQWMACANKGY	448
Db	353	RANCNKIIMLFTDGGEERAQEIFAQYN-KDKKVRVFTFSVGQHNYDRGPIQWMACENKGY	411
Qy	449	YFEIPSIGAIRINTQEYLDVLGRPMVLAGEAKQVQWNTNVEDALGLGLVVTGTLPVFNL	508
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Qy	509	TQ--DGPGEKKNLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKP	566
Db	472	TGQFENKTNLKNQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQP	531
Qy	567	Q-----TTNFR-----EPVTLDFLDAELEEDENKEEIRRSMDGNKGHKQIR	607
Db	532	KPIGVGIPTINLRKRRPNVQNPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFR	591
Qy	608	TLVKSLDERYIDEVTRNYTWVPIRSTNY-SLGLVLPPYSTFYQLQANLSDQILQVKYFEFL	666
Db	592	TLVKSQDERYIDKGNRTYTWTVPVNGTDYSSLALVLPTYSFYIYKAKIEETITQARYSETL	651
Qy	667	LPSSFESSEGHVFIAPREYCKDLNASDNNTFELKNFIELMEKVTPDSKQCNNFLLHNLILD	726
Db	652	KPDNFEESGYTFLAPRDYCSDLKPSDNNTFELNLFNEFIDRKTPNNPSCNTDLINRVLLD	711
Qy	727	TGITQQLVERVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPEPFNASFYRRS	786
Db	712	AGFTNELVQNYWSKQK-NIKGVKARFVVTDDGGITRVYPKEAGENWQENPETYEDSFYKRS	770
Qy	787	LDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRLPAVVGKLDLEAWAE	846
Db	771	LDNDNYVFTAPYFNK-SGPGAYES---GIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIE	826
Qy	847	KFKVLASNRTHQDQPKC-GPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQWDQVG	905
Db	827	NF-----TKTSIRD--CAGP----VCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIG	875
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Db	876	RFFGEIDPSLMRHLVNI SVYAFNKS YDYSVCEPGAAPKQGAGHRSAYVPSIADILQIGW	935
Qy	966	WTSAAAWSLFQQLLYGLIYHSWFQ-ADPAEAEAGSPETRESSCVMKQTQYYFGSVNASYNA	1024
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Qy	1025	IIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCELVQRP	1084
Db	996	VLD CGNCSRI FHVEKLMNTNLIFIMVESKGTCPCDTRLIIQAEQ--TSDGPDPCDMVKQP	1053
Qy	1085	RYRRGPHICFDYNATEDTSDCG	1106
Db	1054	RYRKGPDVCFDNNVLEDYTDG	1075

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 13, 2006, 02:38:55 ; Search time 11976 Seconds  
(without alignments)  
5263.810 Million cell updates/sec

Title: US-10-088-876-6  
Perfect score: 5911  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*

13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	5911	100.0	5463	6	AR225038	AR225038 Sequence
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23	5716	96.7	5498	9	AF247139	AF247139 Mus muscu
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27	5678	96.1	3561	9	AY502107	AY502107 Mus muscu
28	5641	95.4	3186	6	AR577710	AR577710 Sequence
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35	5113	86.5	3052	6	CQ716401	CQ716401 Sequence
36	3077.5	52.1	3882	9	MMU73487	U73487 Mus musculu
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38	3065	51.9	3939	9	MMU73483	U73483 Mus musculu
39	3058	51.7	3903	9	MMU73484	U73484 Mus musculu
40	3050.5	51.6	3965	9	AF286488	AF286488 Rattus no
41	3048.5	51.6	3888	9	MMU73485	U73485 Mus musculu
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44	3045	51.5	3802	6	I40162	I40162 Sequence 2

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I73185 Sequence 2

# ALIGNMENTS

## RESULT 1

AR577712

LOCUS AR577712 3327 bp DNA linear PAT 14-DEC-2004

DEFINITION Sequence 3 from patent US 6783952.

ACCESSION AR577712

VERSION AR577712.1 GI:56580355

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 3327)

AUTHORS Brown,J.P. and Bertelli,F.

TITLE Secreted soluble .alpha.2.delta.-2, .alpha.2.delta.-3 or .alpha.2.delta.-4 calcium channel subunit polypeptides and screening assays using same

JOURNAL Patent: US 6783952-A 3 31-AUG-2004;  
Warner-Lambert Company; Morris Plains, NJ

FEATURES Location/Qualifiers

source 1..3327  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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US-10-088-876-6 (1-1109) x AR577712 (1-3327)

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Db      1 ATGGCGGTGCCGGCTCGGACCTGCGGCGCCTCTCGGCCCGGCCAGCGCGGACTGCGCGC 60

Qy     21 ProTrpProGlyCysGlyProHisProGlyProGlyThrArgArgProThrSerGlyPro 40
          |||
Db     61 CCCTGGCCCCGGCTGCGGCCCCACCTGGCCCCGGCACCCGGCGCCCGACGTCCGGGCCC 120

Qy     41 ProArgProLeuTrpLeuLeuLeuProLeuLeuProLeuLeuAlaAlaProGlyAlaSer 60
          |||
Db    121 CCGCGCCCGCTGTGGCTGCTGCTGCCGCTTCTACCGCTGCTCGCCGCCCCGGCGCCTCT 180

Qy     61 AlaTyrSerPheProGlnGlnHisThrMetGlnHisTrpAlaArgArgLeuGluGlnGlu 80
          |||
Db    181 GCCTACAGCTTCCCCAGCAGCACACGATGCAGCACTGGGCCCGGCGTCTGGAGCAGGAG 240

Qy     81 ValAspGlyValMetArgIlePheGlyGlyValGlnGlnLeuArgGluIleTyrLysAsp 100
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Db	361	GGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAGGCCCTGAAGAGACTGGCTGATGCT	420
Qy	141	AlaGluAsnPheGlnLysAlaHisArgTrpGlnAspAsnIleLysGluGluAspIleVal	160
Db	421	GCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGACAACATCAAGGAGGAAGACATCGTG	480
Qy	161	TyrTyrAspAlaLysAlaAspAlaGluLeuAspAspProGluSerGluAspValGluArg	180
Db	481	TACTATGACGCCAAGGCTGACGCTGAGCTGGACGACCCTGAGAGTGAGGATGTGGAAAGG	540
Qy	181	GlySerLysAlaSerThrLeuArgLeuAspPheIleGluAspProAsnPheLysAsnLys	200
Db	541	GGGTCTAAGGCCAGCACCCCTAAGGCTGGACTTCATCGAGGACCCAAACTTCAAGAACAAG	600
Qy	201	ValAsnTyrSerTyrAlaAlaValGlnIleProThrAspIleTyrLysGlySerThrVal	220
Db	601	GTCAACTATTTCATACGCGGCTGTACAGATCCCTACGGACATCTACAAAGGCTCCACTGTC	660
Qy	221	IleLeuAsnGluLeuAsnTrpThrGluAlaLeuGluAsnValPheMetGluAsnArgArg	240
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Db	781	CCGGCCACCCCGTGGCGAGCCCCCAAGAAGATCGACCTGTACGATGTCCGAAGGAGACCC	840
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Qy	321	LeuSerAspAspAspTyrValAsnValAlaSerPheAsnGluLysAlaGlnProValSer	340
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Qy	361	GlnGlyMetValAlaLysGlyThrThrGlyTyrLysAlaGlyPheGluTyrAlaPheAsp	380
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Qy	381	GlnLeuGlnAsnSerAsnIleThrArgAlaAsnCysAsnLysMetIleMetMetPheThr	400
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Qy	401	AspGlyGlyGluAspArgValGlnAspValPheGluLysTyrAsnTrpProAsnArgThr	420
Db	1201	 GATGGTGGTGAGGACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACG	1260
Qy	421	ValArgValPheThrPheSerValGlyGlnHisAsnTyrAspValThrProLeuGlnTrp	440
Db	1261	 GTGCGCGTGTTTACTTTCTCCGTGGGGCAGCATAACTATGACGTACACCGCTGCAGTGG	1320
Qy	441	MetAlaCysAlaAsnLysGlyTyrTyrPheGluIleProSerIleGlyAlaIleArgIle	460
Db	1321	 ATGGCCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATC	1380
Qy	461	AsnThrGlnGluTyrLeuAspValLeuGlyArgProMetValLeuAlaGlyLysGluAla	480
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Qy	501	GlyThrLeuProValPheAsnLeuThrGlnAspGlyProGlyGluLysLysAsnGlnLeu	520
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Qy	601	LysGlyHisLysGlnIleArgThrLeuValLysSerLeuAspGluArgTyrIleAspGlu	620
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 13, 2006, 03:00:48 ; Search time 8617 Seconds  
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	3026.5	51.2	6323	4	CR857577	CR857577	Pongo pyg
5	2992.5	50.6	2753	10	AY403435	AY403435	Pan trogl
6	2687.5	45.5	3675	4	AK014825	AK014825	Mus muscu
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8	2308	39.0	3178	10	AY406386	AY406386	Homo sapi
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13	1307	22.1	744	8	CX562191	CX562191	UI-M-FC0-
14	1272	21.5	762	6	CD348913	CD348913	UI-M-FY0-
c 15	1259	21.3	709	8	DN880322	DN880322	nae33c05.
16	1257.5	21.3	1114	8	DN708930	DN708930	CLJ80-C11
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19	1199	20.3	688	6	CD578971	CD578971	UI-M-FY0-
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29	1095.5	18.5	794	8	DR425655	DR425655	naw21c07.
30	1081	18.3	641	6	CD348021	CD348021	UI-M-FY0-
31	1076	18.2	636	3	BQ042167	BQ042167	UI-M-EQ0-
32	1071	18.1	804	8	CX794932	CX794932	JGI_CAAJ1
33	1061.5	18.0	967	5	BY714348	BY714348	BY714348
34	1049.5	17.8	886	5	BX704606	BX704606	BX704606
35	1027.5	17.4	679	6	CF534715	CF534715	UI-M-GH0-
36	1022	17.3	598	5	BQ443630	BQ443630	UI-M-EW0-
37	1021	17.3	729	6	CD349156	CD349156	UI-M-FY0-
38	1018.5	17.2	812	8	CX895201	CX895201	JGI_CAAM6
39	1010	17.1	819	8	CX794146	CX794146	JGI_CAAJ6
40	1004	17.0	580	7	CN294018	CN294018	170005322
41	1003	17.0	587	5	BU708875	BU708875	UI-M-FI0-
42	1002	17.0	588	3	BP250236	BP250236	BP250236
43	1002	17.0	672	6	CA749445	CA749445	UI-M-FY0-
44	990.5	16.8	702	6	CD493764	CD493764	CDA07-A03
45	983.5	16.6	764	6	CB235092	CB235092	AGENCOURT

# ALIGNMENTS

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 11, 2006, 01:00:26 ; Search time 185 Seconds  
 (without alignments)  
 2504.717 Million cell updates/sec

Title: US-10-088-876-6  
 Perfect score: 5911  
 Sequence: 1 MAVPARTCGASRPGPARTAR.....PHICFDYNATEDTSDCGRGA 1109

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	5911	100.0	1109	5	US-10-902-531-6	Sequence 6, Appli
2	5911	100.0	1115	5	US-10-902-531-23	Sequence 23, Appl
3	5911	100.0	1145	4	US-10-116-949-2	Sequence 2, Appli
4	5911	100.0	1145	4	US-10-116-949-4	Sequence 4, Appli
5	5911	100.0	1145	5	US-10-723-860-1799	Sequence 1799, Ap
6	5911	100.0	1145	5	US-10-482-029-114	Sequence 114, App
7	5911	100.0	1145	5	US-10-902-531-20	Sequence 20, Appl
8	5873	99.4	1141	5	US-10-417-375-174	Sequence 174, App
9	5862.5	99.2	1142	5	US-10-417-375-172	Sequence 172, App
10	5843	98.8	1139	5	US-10-417-375-176	Sequence 176, App
11	5753	97.3	1082	5	US-10-902-531-5	Sequence 5, Appli

12	5716	96.7	1156	5	US-10-823-432-32	Sequence 32, Appl
13	5712	96.6	1148	5	US-10-823-432-36	Sequence 36, Appl
14	5704	96.5	1150	5	US-10-924-081-3	Sequence 3, Appli
15	5693	96.3	1152	5	US-10-417-375-169	Sequence 169, App
16	5686.5	96.2	1157	5	US-10-924-081-1	Sequence 1, Appli
17	5686.5	96.2	1157	5	US-10-823-432-33	Sequence 33, Appl
18	5686.5	96.2	1157	5	US-10-823-432-34	Sequence 34, Appl
19	5682.5	96.1	1157	5	US-10-924-081-11	Sequence 11, Appl
20	5641	95.4	1062	5	US-10-902-531-4	Sequence 4, Appli
21	5551.5	93.9	1098	5	US-10-823-432-35	Sequence 35, Appl
22	5519	93.4	1076	4	US-10-116-949-6	Sequence 6, Appli
23	3045	51.5	1084	5	US-10-823-447-29	Sequence 29, Appl
24	3045	51.5	1084	5	US-10-823-432-29	Sequence 29, Appl
25	3035.5	51.4	1079	5	US-10-823-447-28	Sequence 28, Appl
26	3035.5	51.4	1079	5	US-10-823-432-28	Sequence 28, Appl
27	3032.5	51.3	1103	5	US-10-823-447-25	Sequence 25, Appl
28	3032.5	51.3	1103	5	US-10-823-432-25	Sequence 25, Appl
29	3025.5	51.2	1063	4	US-10-090-827-8	Sequence 8, Appli
30	3025.5	51.2	1063	5	US-10-901-503-8	Sequence 8, Appli
31	3025.5	51.2	1063	6	US-11-114-581-8	Sequence 8, Appli
32	3025.5	51.2	1069	4	US-10-090-827-9	Sequence 9, Appli
33	3025.5	51.2	1069	6	US-11-114-581-9	Sequence 9, Appli
34	3025.5	51.2	1091	4	US-10-090-827-5	Sequence 5, Appli
35	3025.5	51.2	1091	5	US-10-823-447-26	Sequence 26, Appl
36	3025.5	51.2	1091	5	US-10-823-447-31	Sequence 31, Appl
37	3025.5	51.2	1091	5	US-10-901-503-5	Sequence 5, Appli
38	3025.5	51.2	1091	5	US-10-823-432-26	Sequence 26, Appl
39	3025.5	51.2	1091	5	US-10-823-432-31	Sequence 31, Appl
40	3025.5	51.2	1091	6	US-11-114-581-5	Sequence 5, Appli
41	3024	51.2	1084	4	US-10-375-253-53	Sequence 53, Appl
42	3020	51.1	1087	5	US-10-918-602-2	Sequence 2, Appli
43	3016	51.0	1086	5	US-10-823-447-27	Sequence 27, Appl
44	3016	51.0	1086	5	US-10-823-432-27	Sequence 27, Appl
45	3014.5	51.0	1079	4	US-10-375-253-51	Sequence 51, Appl

# ALIGNMENTS

## RESULT 1

US-10-902-531-6

; Sequence 6, Application US/10902531

; Publication No. US20050042659A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2

; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and

; TITLE OF INVENTION: screening assays using same

; FILE REFERENCE: 180

; CURRENT APPLICATION NUMBER: US/10/902,531

; CURRENT FILING DATE: 2004-07-29

; PRIOR APPLICATION NUMBER: US/09/397,550

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 1109

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-902-531-6

Query Match 100.0%; Score 5911; DB 5; Length 1109;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLLPLLPLLAAPGAS	60
Db	1	MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLLPLLPLLAAPGAS	60
Qy	61	AYSFPQOHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVA	120
Db	61	AYSFPQOHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVA	120
Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNR	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNR	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTVNYEDALGLGLVVTGTLPVFNLTDGPGGEKKNQLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTVNYEDALGLGLVVTGTLPVFNLTDGPGGEKKNQLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSIDGN	600
Db	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSIDGN	600
Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPYSTFYQLQANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPYSTFYQLQANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Qy	721	HNLILDTGITQQQLVERVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780

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Db      721 HNLILDTGITQQLVERVWRDQDLNTYSL LAVFAATDGGITRVFPNKAEDWTENPEPFNA 780
Qy      781 SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTL RPAVVGVKLD 840
Db      781 SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTL RPAVVGVKLD 840
Qy      841 LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNE DLLCVLIDDGGFLVLSNQNHQ 900
Db      841 LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNE DLLCVLIDDGGFLVLSNQNHQ 900
Qy      901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF 960
Db      901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADF 960
Qy      961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020
Db      961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020
Qy      1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080
Db      1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080
Qy      1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109
Db      1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109

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RESULT 2

US-10-902-531-23

; Sequence 23, Application US/10902531

; Publication No. US20050042659A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2

; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and

; TITLE OF INVENTION: screening assays using same

; FILE REFERENCE: 180

; CURRENT APPLICATION NUMBER: US/10/902,531

; CURRENT FILING DATE: 2004-07-29

; PRIOR APPLICATION NUMBER: US/09/397,550

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 1115

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-902-531-23

Query Match 100.0%; Score 5911; DB 5; Length 1115;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAVPARTCGASRPGPARTARPWPGCGPHPGPTRRPTSGPPRPLWLLLPLLLAAPGAS 60
Db      1 MAVPARTCGASRPGPARTARPWPGCGPHPGPTRRPTSGPPRPLWLLLPLLLAAPGAS 60

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Db	61	AYSFPQQHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVA	120
Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTNVYEDALGLGLVVTGTLPVFNLTQDGPGEKKNLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRSMIDGN	600
Db	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRSMIDGN	600
Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLGLVLPYSTFYLANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLGLVLPYSTFYLANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Qy	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Db	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Qy	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Db	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Qy	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900
Db	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900



Qy 901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960  
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 Db 901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960

Qy 961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020  
 |||  
 Db 961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAEGSPETRESSCVMKQTQYYFGSVNA 1020

Qy 1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080  
 |||  
 Db 1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080

Qy 1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109  
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 Db 1081 VQRPRYRRGPHICFDYNATEDTSDCGRGA 1109

RESULT 3

US-10-116-949-2

; Sequence 2, Application US/10116949  
 ; Publication No. US20030044911A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lerman, Michael I.  
 ; APPLICANT: Minna, John D.  
 ; APPLICANT: Latif, Farida  
 ; APPLICANT: Wei, Ming-Hui  
 ; APPLICANT: Sekido, Yoshitaka  
 ; APPLICANT: Gao, Boning  
 ; APPLICANT: Duh, Fuh-Mei  
 ; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof  
 ; FILE REFERENCE: NIH-05043  
 ; CURRENT APPLICATION NUMBER: US/10/116,949  
 ; CURRENT FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1145  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-116-949-2

Query Match 100.0%; Score 5911; DB 4; Length 1145;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAVPARTCGASRPGPARTARWPWPGCGPHPGPTRRPTSGPPRPLWLLLPLLLAAPGAS 60  
 |||  
 Db 1 MAVPARTCGASRPGPARTARWPWPGCGPHPGPTRRPTSGPPRPLWLLLPLLLAAPGAS 60

Qy 61 AYSFPQOHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQENEPQKLVEKVA 120  
 |||  
 Db 61 AYSFPQOHTMQHWARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFQENEPQKLVEKVA 120

Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Qy	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Db	181	GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240
Qy	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Db	241	QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG	300
Qy	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Db	301	SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV	360
Qy	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNT	420
Db	361	QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMFTDGGEDRVQDVFKEYNWPNT	420
Qy	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Db	421	VRVFTFSVGQHNYDVTPLQWMACANKGYFFEIPSIGAIRINTQEYLDVLGRPMVLAGEA	480
Qy	481	KQVQWTVNYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Db	481	KQVQWTVNYEDALGLGLVVTGTLPVFNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPN	540
Qy	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSMDGN	600
Db	541	YTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTLDFLDAELEDENKEEIRRSMDGN	600
Qy	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLGLVLPYSTFYQLQANLSDQILQV	660
Db	601	KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLGLVLPYSTFYQLQANLSDQILQV	660
Qy	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Db	661	KYFEFLLPSSFESSEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL	720
Qy	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Db	721	HNLILDTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA	780
Qy	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Db	781	SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRAVVGVKLD	840
Qy	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900
Db	841	LEAWAEKFKVLASNRTHQDQPQKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ	900
Qy	901	WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF	960
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RESULT 4

US-10-116-949-4

; Sequence 4, Application US/10116949

; Publication No. US20030044911A1

; GENERAL INFORMATION:

; APPLICANT: Lerman, Michael I.

; APPLICANT: Minna, John D.

; APPLICANT: Latif, Farida

; APPLICANT: Wei, Ming-Hui

; APPLICANT: Sekido, Yoshitaka

; APPLICANT: Gao, Boning

; APPLICANT: Duh, Fuh-Mei

; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof

; FILE REFERENCE: NIH-05043

; CURRENT APPLICATION NUMBER: US/10/116,949

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1145

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-116-949-4

Query Match 100.0%; Score 5911; DB 4; Length 1145;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          121 GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER 180
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Db          121 GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER 180

Qy          181 GSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR 240

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

# SUMMARIES

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1	5911	100.0	3327	3	US-09-397-550-3	Sequence 3, Appli
2	5911	100.0	5463	3	US-09-470-443-1	Sequence 1, Appli
3	5911	100.0	5482	3	US-09-470-443-3	Sequence 3, Appli
4	5911	100.0	5482	3	US-09-397-550-19	Sequence 19, Appl
5	5753	97.3	3248	3	US-09-397-550-2	Sequence 2, Appli
6	5641	95.4	3186	3	US-09-397-550-1	Sequence 1, Appli
7	5533.5	93.6	5279	3	US-09-470-443-5	Sequence 5, Appli
8	3047	51.5	3802	2	US-08-336-257A-4	Sequence 4, Appli
9	3045	51.5	3802	2	US-08-404-354B-2	Sequence 2, Appli
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13	3025.5	51.2	3192	3	US-10-090-827-4	Sequence 4, Appli
14	3025.5	51.2	3192	3	US-09-397-548-4	Sequence 4, Appli
15	3025.5	51.2	3842	3	US-10-090-827-1	Sequence 1, Appli
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17	3024	51.2	3579	2	US-08-455-543A-36	Sequence 36, Appl
18	3024	51.2	3579	2	US-08-193-078B-25	Sequence 25, Appl
19	3024	51.2	3579	2	US-08-223-305C-36	Sequence 36, Appl
20	3024	51.2	3579	3	US-08-949-386-32	Sequence 32, Appl
21	3024	51.2	3579	3	US-08-450-562-32	Sequence 32, Appl
22	3024	51.2	3579	3	US-08-984-709A-32	Sequence 32, Appl
23	3024	51.2	3579	3	US-08-450-272-32	Sequence 32, Appl
24	3024	51.2	3579	3	US-08-450-273-32	Sequence 32, Appl
25	3014.5	51.0	3564	2	US-08-455-543A-35	Sequence 35, Appl
26	3014.5	51.0	3564	2	US-08-193-078B-24	Sequence 24, Appl
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28	3014.5	51.0	3564	3	US-08-949-386-31	Sequence 31, Appl
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30	3014.5	51.0	3564	3	US-08-984-709A-31	Sequence 31, Appl
31	3014.5	51.0	3564	3	US-08-450-272-31	Sequence 31, Appl
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33	3012	51.0	3802	9	5386025-7	Patent No. 5386025
34	3011.5	50.9	3636	2	US-08-455-543A-32	Sequence 32, Appl
35	3011.5	50.9	3636	2	US-08-193-078B-22	Sequence 22, Appl
36	3011.5	50.9	3636	2	US-08-223-305C-32	Sequence 32, Appl
37	3011.5	50.9	3636	3	US-08-949-386-29	Sequence 29, Appl
38	3011.5	50.9	3636	3	US-08-450-562-29	Sequence 29, Appl
39	3011.5	50.9	3636	3	US-08-984-709A-29	Sequence 29, Appl
40	3011.5	50.9	3636	3	US-08-450-272-29	Sequence 29, Appl
41	3011.5	50.9	3636	3	US-08-450-273-29	Sequence 29, Appl
42	3004.5	50.8	3190	3	US-10-090-827-12	Sequence 12, Appl
43	3004.5	50.8	3190	3	US-09-397-548-21	Sequence 21, Appl
44	3004.5	50.8	3566	2	US-07-745-206A-24	Sequence 24, Appl
45	3004.5	50.8	3566	2	US-08-311-363-24	Sequence 24, Appl

# ALIGNMENTS

RESULT 1

US-09-397-550-3

; Sequence 3, Application US/09397550

; Patent No. 6783952

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2

; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and

; TITLE OF INVENTION: screening assays using same

; FILE REFERENCE: 180

; CURRENT APPLICATION NUMBER: US/09/397,550

; CURRENT FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 3327

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-397-550-3

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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Qy	21	ProTrpProGlyCysGlyProHisProGlyProGlyThrArgArgProThrSerGlyPro	40
Db	61	CCCTGGCCCGGCTGCGGCCCCACCCTGGCCCCGGCACCCGGCGCCCCAGCTCCGGGCCC	120
Qy	41	ProArgProLeuTrpLeuLeuLeuProLeuLeuProLeuLeuAlaAlaProGlyAlaSer	60
Db	121	CCGCGCCCGCTGTGGCTGCTGCTGCGGCTTCTACCGCTGCTCGCCGCCCGGCGCCTCT	180
Qy	61	AlaTyrSerPheProGlnGlnHisThrMetGlnHisTrpAlaArgArgLeuGluGlnGlu	80
Db	181	GCCTACAGCTTCCCCAGCAGCACACGATGCAGCACTGGGCCCGGCGTCTGGAGCAGGAG	240
Qy	81	ValAspGlyValMetArgIlePheGlyGlyValGlnGlnLeuArgGluIleTyrLysAsp	100
Db	241	GTCGACGGCGTGATGCGGATTTTGGAGGCGTCCAGCAGCTCCGTGAGATTTACAAGGAC	300
Qy	101	AsnArgAsnLeuPheGluValGlnGluAsnGluProGlnLysLeuValGluLysValAla	120
Db	301	AACCGGAACCTGTTTCAGAGTACAGGAGAATGAGCCTCAGAAGTTGGTGGAGAAGGTGGCA	360
Qy	121	GlyAspIleGluSerLeuLeuAspArgLysValGlnAlaLeuLysArgLeuAlaAspAla	140
Db	361	GGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAGGCCCTGAAGAGACTGGCTGATGCT	420

Qy	141	AlaGluAsnPheGlnLysAlaHisArgTrpGlnAspAsnIleLysGluGluAspIleVal	160
Db	421	GCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGACAACATCAAGGAGGAAGACATCGTG	480
Qy	161	TyrTyrAspAlaLysAlaAspAlaGluLeuAspAspProGluSerGluAspValGluArg	180
Db	481	TACTATGACGCCAAGGCTGACGCTGAGCTGGACGACCCTGAGAGTGAGGATGTGGAAAGG	540
Qy	181	GlySerLysAlaSerThrLeuArgLeuAspPheIleGluAspProAsnPheLysAsnLys	200
Db	541	GGGTCTAAGGCCAGCACCTAAGGCTGGACTTCATCGAGGACCCAACTTCAAGAACAG	600
Qy	201	ValAsnTyrSerTyrAlaAlaValGlnIleProThrAspIleTyrLysGlySerThrVal	220
Db	601	GTCAACTATTTCATACGCGGCTGTACAGATCCCTACGGACATCTACAAAGGCTCCACTGTC	660
Qy	221	IleLeuAsnGluLeuAsnTrpThrGluAlaLeuGluAsnValPheMetGluAsnArgArg	240
Db	661	ATCCTCAATGAGCTCAACTGGACAGAGGCCCTGGAGAATGTGTTTCATGGAAAACCGCAGA	720
Qy	241	GlnAspProThrLeuLeuTrpGlnValPheGlySerAlaThrGlyValThrArgTyrTyr	260
Db	721	CAAGACCCACACTGCTGTGGCAGGTCTTCGGCAGCGCCACAGGAGTCACTCGCTACTAC	780
Qy	261	ProAlaThrProTrpArgAlaProLysLysIleAspLeuTyrAspValArgArgArgPro	280
Db	781	CCGGCCACCCCGTGGCGAGCCCCAAGAAGATCGACCTGTACGATGTCCGAAGGAGACCC	840
Qy	281	TrpTyrIleGlnGlyAlaSerSerProLysAspMetValIleIleValAspValSerGly	300
Db	841	TGGTATATCCAGGGGGCCTCGTCACCCAAAGACATGGTCATCATCGTGGATGTGAGTGGC	900
Qy	301	SerValSerGlyLeuThrLeuLysLeuMetLysThrSerValCysGluMetLeuAspThr	320
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Qy	361	GlnGlyMetValAlaLysGlyThrThrGlyTyrLysAlaGlyPheGluTyrAlaPheAsp	380
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Qy	381	GlnLeuGlnAsnSerAsnIleThrArgAlaAsnCysAsnLysMetIleMetMetPheThr	400
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Qy	401	AspGlyGlyGluAspArgValGlnAspValPheGluLysTyrAsnTrpProAsnArgThr	420
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Qy	421	ValArgValPheThrPheSerValGlyGlnHisAsnTyrAspValThrProLeuGlnTrp	440

Db	1261	 GTGCGCGTGTTTACTTTCTCCGTGGGGCAGCATAACTATGACGTCACACCGCTGCAGTGG	1320
Qy	441	MetAlaCysAlaAsnLysGlyTyrTyrPheGluIleProSerIleGlyAlaIleArgIle	460
Db	1321	 ATGGCCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATC	1380
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Qy	481	LysGlnValGlnTrpThrAsnValTyrGluAspAlaLeuGlyLeuGlyLeuValValThr	500
Db	1441	 AAGCAGGTTCACTGGACCAACGTGTATGAGGATGCACTGGGACTGGGGTTGGTGGTAACA	1500
Qy	501	GlyThrLeuProValPheAsnLeuThrGlnAspGlyProGlyGluLysLysAsnGlnLeu	520
Db	1501	 GGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGAAAAGAAGAACCAGCTG	1560
Qy	521	IleLeuGlyValMetGlyIleAspValAlaLeuAsnAspIleLysArgLeuThrProAsn	540
Db	1561	 ATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAATGACATCAAGAGGCTGACCCCCAAC	1620
Qy	541	TyrThrLeuGlyAlaAsnGlyTyrValPheAlaIleAspLeuAsnGlyTyrValLeuLeu	560
Db	1621	 TACACGCTTGGAGCCAACGGCTATGTGTTTGCCATTGACCTGAACGGCTACGTGTTGCTG	1680
Qy	561	HisProAsnLeuLysProGlnThrThrAsnPheArgGluProValThrLeuAspPheLeu	580
Db	1681	 CACCCCAATCTCAAGCCCCAGACCACCAACTTCCGGGAGCCTGTGACTCTGGACTTCCTG	1740
Qy	581	AspAlaGluLeuGluAspGluAsnLysGluGluIleArgArgSerMetIleAspGlyAsn	600
Db	1741	 GATGCGGAGCTAGAGGATGAGAACAAGGAAGAGATCCGTGCGGAGCATGATTGATGGCAAC	1800
Qy	601	LysGlyHisLysGlnIleArgThrLeuValLysSerLeuAspGluArgTyrIleAspGlu	620
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Qy	621	ValThrArgAsnTyrThrTrpValProIleArgSerThrAsnTyrSerLeuGlyLeuVal	640
Db	1861	 GTGACACGGAATAACCTGGGTGCCTATAAGGAGCACTAACTACAGCCTGGGGCTGGTG	1920
Qy	641	LeuProProTyrSerThrPheTyrLeuGlnAlaAsnLeuSerAspGlnIleLeuGlnVal	660
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Qy	701	PheIleGluLeuMetGluLysValThrProAspSerLysGlnCysAsnAsnPheLeuLeu	720



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Qy	821	ValGluLeuSerLeuGlyArgArgThrLeuArgProAlaValValGlyValLysLeuAsp	840
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Qy	921	AsnAsnSerPheTyrThrArgLysGluSerTyrAspTyrGlnAlaAlaCysAlaProGln	940
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Qy	941	ProProGlyAsnLeuGlyAlaAlaProArgGlyValPheValProThrValAlaAspPhe	960
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Qy	981	GlyLeuIleTyrHisSerTrpPheGlnAlaAspProAlaGluAlaGluGlySerProGlu	1000
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 Db 3001 ACGCGCGAGAGCAGCTGCGTCATGAAACAGACCCAGTACTACTTCGGCTCGGTAAACGCC 3060  
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 Db 3061 TCCTACAACGCCATCATCGACTGCGGAACTGCTCCAGGCTGTTCCACGCGCAGAGACTG 3120  
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 Db 3241 GTGCAGAGACCGCGATACCGGAGAGGCCCGCACATCTGCTTCGACTACAACGCGACAGAA 3300  
 Qy 1101 AspThrSerAspCysGlyArgGlyAla 1109  
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 Db 3301 GATACCTCAGACTGTGGCCGCGGGGCC 3327

# RESULT 2

US-09-470-443-1

; Sequence 1, Application US/09470443

; Patent No. 6441156

; GENERAL INFORMATION:

; APPLICANT: Lerman, Michael I.

; APPLICANT: Minna, John D.

; APPLICANT: Latif, Farida

; APPLICANT: Wei, Ming-Hui

; APPLICANT: Sekido, Yoshitaka

; APPLICANT: Gao, Boning

; APPLICANT: Duh, Fuh-Mei

; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof

; FILE REFERENCE: NIH-05043

; CURRENT APPLICATION NUMBER: US/09/470,443

; CURRENT FILING DATE: 1999-12-22

; EARLIER APPLICATION NUMBER: 60/114,359

; EARLIER FILING DATE: 1998-12-30

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 5463

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (162)..(3599)

US-09-470-443-1

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US-10-088-876-6 (1-1109) x US-09-470-443-1 (1-5463)

Qy	1	MetAlaValProAlaArgThrCysGlyAlaSerArgProGlyProAlaArgThrAlaArg	20
Db	162	ATGGCGGTGCCGGCTCGGACCTGCGGCGCCTCTCGGCCCGGCCAGCGCGGACTGCGCGC	221
Qy	21	ProTrpProGlyCysGlyProHisProGlyProGlyThrArgArgProThrSerGlyPro	40
Db	222	CCCTGGCCCGGCTGCGGCCCCACCCTGGCCCCGGCACCCGGCGCCCGACGTCCGGGCCC	281
Qy	41	ProArgProLeuTrpLeuLeuLeuProLeuLeuProLeuLeuAlaAlaProGlyAlaSer	60
Db	282	CCGCGCCCGCTGTGGCTGCTGCTGCCGCTTCTACCGCTGCTCGCCGCCCGGGCGCCTCT	341
Qy	61	AlaTyrSerPheProGlnGlnHisThrMetGlnHisTrpAlaArgArgLeuGluGlnGlu	80
Db	342	GCCTACAGCTTCCCCAGCAGCACACGATGCAGCACTGGGCCCGGCGTCTGGAGCAGGAG	401
Qy	81	ValAspGlyValMetArgIlePheGlyGlyValGlnGlnLeuArgGluIleTyrLysAsp	100
Db	402	GTCGACGGCGTGATGCGGATTTTTGGAGGCGTCCAGCAGCTCCGTGAGATTTACAAGGAC	461
Qy	101	AsnArgAsnLeuPheGluValGlnGluAsnGluProGlnLysLeuValGluLysValAla	120
Db	462	AACCGGAACCTGTTTCGAGGTACAGGAGAATGAGCCTCAGAAGTTGGTGGAGAAGGTGGCA	521
Qy	121	GlyAspIleGluSerLeuLeuAspArgLysValGlnAlaLeuLysArgLeuAlaAspAla	140
Db	522	GGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAGGCCCTGAAGAGACTGGCTGATGCT	581
Qy	141	AlaGluAsnPheGlnLysAlaHisArgTrpGlnAspAsnIleLysGluGluAspIleVal	160
Db	582	GCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGACAACATCAAGGAGGAAGACATCGTG	641
Qy	161	TyrTyrAspAlaLysAlaAspAlaGluLeuAspAspProGluSerGluAspValGluArg	180
Db	642	TACTATGACGCCAAGGCTGACGCTGAGCTGGACGACCCTGAGAGTGAGGATGTGGAAAGG	701
Qy	181	GlySerLysAlaSerThrLeuArgLeuAspPheIleGluAspProAsnPheLysAsnLys	200
Db	702	GGGTCTAAGGCCAGCACCTAAGGCTGGACTTCATCGAGGACCCAACTTCAAGAACAAG	761
Qy	201	ValAsnTyrSerTyrAlaAlaValGlnIleProThrAspIleTyrLysGlySerThrVal	220
Db	762	GTCAACTATTACATACGCGGCTGTACAGATCCCTACGGACATCTACAAAGGCTCCACTGTC	821
Qy	221	IleLeuAsnGluLeuAsnTrpThrGluAlaLeuGluAsnValPheMetGluAsnArgArg	240
Db	822	ATCCTCAATGAGCTCAACTGGACAGAGGCCCTGGAGAATGTGTTTCATGGAAAACCGCAGA	881
Qy	241	GlnAspProThrLeuLeuTrpGlnValPheGlySerAlaThrGlyValThrArgTyrTyr	260

Db	882	CAAGACCCACACTGCTGTGGCAGGTCTTCGGCAGCGCCACAGGAGTCACTCGCTACTAC	941
Qy	261	ProAlaThrProTrpArgAlaProLysLysIleAspLeuTyrAspValArgArgArgPro	280
Db	942	CCGGCCACCCCGTGGCGAGCCCCAAGAAGATCGACCTGTACGATGTCCGAAGGAGACCC	1001
Qy	281	TrpTyrIleGlnGlyAlaSerSerProLysAspMetValIleIleValAspValSerGly	300
Db	1002	TGGTATATCCAGGGGGCCTCGTCACCCAAAGACATGGTCATCATCGTGGATGTGAGTGGC	1061
Qy	301	SerValSerGlyLeuThrLeuLysLeuMetLysThrSerValCysGluMetLeuAspThr	320
Db	1062	AGTGTGAGCGGCCTGACCCTGAAGCTGATGAAGACATCTGTCTGCGAGATGCTGGACACG	1121
Qy	321	LeuSerAspAspAspTyrValAsnValAlaSerPheAsnGluLysAlaGlnProValSer	340
Db	1122	CTGTCTGATGATGACTATGTGAATGTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA	1181
Qy	341	CysPheThrHisLeuValGlnAlaAsnValArgAsnLysLysValPheLysGluAlaVal	360
Db	1182	TGCTTCACACACCTGGTGCAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTG	1241
Qy	361	GlnGlyMetValAlaLysGlyThrThrGlyTyrLysAlaGlyPheGluTyrAlaPheAsp	380
Db	1242	CAGGGCATGGTGGCCAAGGGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGAC	1301
Qy	381	GlnLeuGlnAsnSerAsnIleThrArgAlaAsnCysAsnLysMetIleMetMetPheThr	400
Db	1302	CAGCTGCAGAACTCCAACATCACTCGGGCCAACTGCAACAAGATGATCATGATGTTACAG	1361
Qy	401	AspGlyGlyGluAspArgValGlnAspValPheGluLysTyrAsnTrpProAsnArgThr	420
Db	1362	GATGGTGGTGAGGACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACG	1421
Qy	421	ValArgValPheThrPheSerValGlyGlnHisAsnTyrAspValThrProLeuGlnTrp	440
Db	1422	GTGCGCGTGTTTACTTTCTCCGTGGGGCAGCATAACTATGACGTCACACCGCTGCAGTGG	1481
Qy	441	MetAlaCysAlaAsnLysGlyTyrTyrPheGluIleProSerIleGlyAlaIleArgIle	460
Db	1482	ATGGCCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATC	1541
Qy	461	AsnThrGlnGluTyrLeuAspValLeuGlyArgProMetValLeuAlaGlyLysGluAla	480
Db	1542	AACACACAGGAATATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAGGAGGCC	1601
Qy	481	LysGlnValGlnTrpThrAsnValTyrGluAspAlaLeuGlyLeuGlyLeuValValThr	500
Db	1602	AAGCAGGTTCAGTGGACCAACGTGTATGAGGATGCACTGGGACTGGGGTTGGTGGTAACA	1661
Qy	501	GlyThrLeuProValPheAsnLeuThrGlnAspGlyProGlyGluLysLysAsnGlnLeu	520
Db	1662	GGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAGAACAGCTG	1721
Qy	521	IleLeuGlyValMetGlyIleAspValAlaLeuAsnAspIleLysArgLeuThrProAsn	540
Db	1722	ATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAATGACATCAAGAGGCTGACCCCCAAC	1781

Qy	541	TyrThrLeuGlyAlaAsnGlyTyrValPheAlaIleAspLeuAsnGlyTyrValLeuLeu	560
Db	1782	TACACGCTTGGAGCCAACGGCTATGTGTTTGCCATTGACCTGAACGGCTACGTGTTGCTG	1841
Qy	561	HisProAsnLeuLysProGlnThrThrAsnPheArgGluProValThrLeuAspPheLeu	580
Db	1842	CACCCAATCTCAAGCCCCAGACCACCAACTTCCGGGAGCCTGTGACTCTGGACTTCCTG	1901
Qy	581	AspAlaGluLeuGluAspGluAsnLysGluGluIleArgArgSerMetIleAspGlyAsn	600
Db	1902	GATGCGGAGCTAGAGGATGAGAACAAGGAAGAGATCCGTCGGAGCATGATTGATGGCAAC	1961
Qy	601	LysGlyHisLysGlnIleArgThrLeuValLysSerLeuAspGluArgTyrIleAspGlu	620
Db	1962	AAGGGCCACAAGCAGATCAGAACGTTGGTCAAGTCCCTGGATGAGAGGTACATAGATGAG	2021
Qy	621	ValThrArgAsnTyrThrTrpValProIleArgSerThrAsnTyrSerLeuGlyLeuVal	640
Db	2022	GTGACACGGAACCTACACCTGGGTGCCTATAAGGAGCACTAACTACAGCCTGGGGCTGGTG	2081
Qy	641	LeuProProTyrSerThrPheTyrLeuGlnAlaAsnLeuSerAspGlnIleLeuGlnVal	660
Db	2082	CTCCACCTACAGCACCTTCTACCTCCAAGCCAATCTCAGTGACCAGATCCTGCAGGTC	2141
Qy	661	LysTyrPheGluPheLeuLeuProSerSerPheGluSerGluGlyHisValPheIleAla	680
Db	2142	AAGTATTTTGAGTTCCTGCTCCCCAGCAGCTTTGAGTCTGAAGGACACGTTTTCATTGCT	2201
Qy	681	ProArgGluTyrCysLysAspLeuAsnAlaSerAspAsnAsnThrGluPheLeuLysAsn	700
Db	2202	CCCAGAGAGTACTGCAAGGACCTGAATGCCTCAGACAACAACACCGAGTTCCTGAAAAC	2261
Qy	701	PheIleGluLeuMetGluLysValThrProAspSerLysGlnCysAsnAsnPheLeuLeu	720
Db	2262	TTTATTGAGCTCATGGAGAAAGTGACTCCAGACTCCAAGCAGTGCAACAACCTCCTTCTG	2321
Qy	721	HisAsnLeuIleLeuAspThrGlyIleThrGlnGlnLeuValGluArgValTrpArgAsp	740
Db	2322	CACAACCTGATCTTGGACACGGGCATCACGCAGCAGCTGGTAGAGCGTGTGTGGAGGGAC	2381
Qy	741	GlnAspLeuAsnThrTyrSerLeuLeuAlaValPheAlaAlaThrAspGlyGlyIleThr	760
Db	2382	CAGGATCTCAACACGTACAGCCTACTGGCCGTGTTGCTGCCACAGACGGTGGCATCACC	2441
Qy	761	ArgValPheProAsnLysAlaAlaGluAspTrpThrGluAsnProGluProPheAsnAla	780
Db	2442	CGAGTCTTCCCAACAAGGCAGCTGAGGACTGGACAGAGAACCCTGAGCCCTTCAATGCC	2501
Qy	781	SerPheTyrArgArgSerLeuAspAsnHisGlyTyrValPheLysProProHisGlnAsp	800
Db	2502	AGCTTCTACCGCCGAGCCTGGATAACCACGGTTATGTCTTCAAGCCCCACACCAGGAT	2561
Qy	801	AlaLeuLeuArgProLeuGluLeuGluAsnAspThrValGlyIleLeuValSerThrAla	820
Db	2562	GCCCTGTTAAGGCCGCTGGAGCTGGAGAATGACACTGTGGGCATCCTCGTCAGCACAGCT	2621

Qy	821	ValGluLeuSerLeuGlyArgArgThrLeuArgProAlaValValGlyValLysLeuAsp	840
Db	2622	GTGGAGCTCAGCCTAGGCAGGCGCACACTGAGGCCAGCAGTGGTGGGCGTCAAGCTGGAC	2681
Qy	841	LeuGluAlaTrpAlaGluLysPheLysValLeuAlaSerAsnArgThrHisGlnAspGln	860
Db	2682	CTAGAGGCTTGGGCTGAGAAGTTCAAGGTGCTAGCCAGCAACCGTACCCACCAAGACCAG	2741
Qy	861	ProGlnLysCysGlyProAsnSerHisCysGluMetAspCysGluValAsnAsnGluAsp	880
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Qy	881	LeuLeuCysValLeuIleAspAspGlyGlyPheLeuValLeuSerAsnGlnAsnHisGln	900
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Qy	901	TrpAspGlnValGlyArgPhePheSerGluValAspAlaAsnLeuMetLeuAlaLeuTyr	920
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Qy	921	AsnAsnSerPheTyrThrArgLysGluSerTyrAspTyrGlnAlaAlaCysAlaProGln	940
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Qy	961	LeuAsnLeuAlaTrpTrpThrSerAlaAlaAlaTrpSerLeuPheGlnGlnLeuLeuTyr	980
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Qy	981	GlyLeuIleTyrHisSerTrpPheGlnAlaAspProAlaGluAlaGluGlySerProGlu	1000
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Db	3282	ACCAACACCAATCTTCTCTTTGTGGTGGCCGAGAAGCCGCTGTGCAGCCAGTGCGAGGCT	3341
Qy	1061	GlyArgLeuLeuGlnLysGluThrHisCysProAlaAspGlyProGluGlnCysGluLeu	1080
Db	3342	GGCCGGCTGCTGCAGAAGGAGACGCACTGCCAGCGGACGGCCCGGAGCAGTGTGAGCTA	3401
Qy	1081	ValGlnArgProArgTyrArgArgGlyProHisIleCysPheAspTyrAsnAlaThrGlu	1100
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Db 3462 GATACCTCAGACTGTGGCCGCGGGGCC 3488

RESULT 3

US-09-470-443-3

; Sequence 3, Application US/09470443

; Patent No. 6441156

; GENERAL INFORMATION:

; APPLICANT: Lerman, Michael I.

; APPLICANT: Minna, John D.

; APPLICANT: Latif, Farida

; APPLICANT: Wei, Ming-Hui

; APPLICANT: Sekido, Yoshitaka

; APPLICANT: Gao, Boning

; APPLICANT: Duh, Fuh-Mei

; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof

; FILE REFERENCE: NIH-05043

; CURRENT APPLICATION NUMBER: US/09/470,443

; CURRENT FILING DATE: 1999-12-22

; EARLIER APPLICATION NUMBER: 60/114,359

; EARLIER FILING DATE: 1998-12-30

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 5482

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (181)..(3618)

US-09-470-443-3

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Db	241	CCCTGGCCCGGCTGCGGCCCCACCCTGGCCCGGCACCCGGCGCCCGACGTCCGGGCCC	300
Qy	41	ProArgProLeuTrpLeuLeuLeuProLeuLeuProLeuLeuAlaAlaProGlyAlaSer	60
Db	301	CCGCGCCCGCTGTGGCTGCTGCTGCCGCTTCTACCGCTGCTCGCCGCCCCGGCGCCTCT	360
Qy	61	AlaTyrSerPheProGlnGlnHisThrMetGlnHisTrpAlaArgArgLeuGluGlnGlu	80
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GenCore version 5.1.7  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	5911	100.0	5303	8	US-10-723-860-1798	Sequence 1798, Ap
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4	5911	100.0	5463	8	US-10-482-029-113	Sequence 113, App
5	5911	100.0	5482	5	US-10-116-949-3	Sequence 3, Appli
6	5911	100.0	5482	8	US-10-902-531-19	Sequence 19, Appl
7	5911	100.0	5730	8	US-10-417-375-173	Sequence 173, App
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9	5881	99.5	4182	8	US-10-417-375-175	Sequence 175, App
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11	5731	97.0	5386	8	US-10-417-375-168	Sequence 168, App
12	5704	96.5	4993	9	US-10-924-081-2	Sequence 2, Appli
13	5689.5	96.3	5583	8	US-10-723-860-6157	Sequence 6157, Ap
14	5682.5	96.1	3474	9	US-10-924-081-10	Sequence 10, Appl
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17	3025.5	51.2	3192	5	US-10-090-827-4	Sequence 4, Appli
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33	2995	50.7	3585	7	US-10-375-253-48	Sequence 48, Appl
34	2959	50.1	7640	6	US-10-062-674-1891	Sequence 1891, Ap
35	2924.5	49.5	3111	5	US-10-090-827-3	Sequence 3, Appli
36	2924.5	49.5	3111	9	US-10-901-503-3	Sequence 3, Appli
37	2924.5	49.5	3111	10	US-11-114-581-3	Sequence 3, Appli
38	2907.5	49.2	3109	5	US-10-090-827-11	Sequence 11, Appl
39	2907.5	49.2	3109	9	US-10-901-503-20	Sequence 20, Appl
40	2907.5	49.2	3109	10	US-11-114-581-11	Sequence 11, Appl
41	2887.5	48.8	3057	5	US-10-090-827-2	Sequence 2, Appli
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43	2887.5	48.8	3057	10	US-11-114-581-2	Sequence 2, Appli
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#### ALIGNMENTS

GenCore version 5.1.7  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10088876/runat\_10022006\_121119\_5218/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p  
-USER=US10088876\_CGN\_1\_1\_1096@runat\_10022006\_121119\_5218 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*

13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	8					
No.	Score	Query Match	Length	DB	ID	Description
1	5911	100.0	3327	4	AAS01406	Aas01406 Human sec
2	5911	100.0	3327	5	AAF57543	Aaf57543 Human cal
3	5911	100.0	4031	12	ADK70361	Adk70361 Respirato
4	5911	100.0	5303	12	ADQ18979	Adq18979 Human sof
5	5911	100.0	5463	6	ABS74267	Abs74267 Human cDN
6	5911	100.0	5463	9	ACD25665	Acd25665 Human cDN
7	5911	100.0	5482	3	AAA09255	Aaa09255 Human alp
8	5911	100.0	5482	4	AAS01413	Aas01413 Human sec
9	5911	100.0	5482	5	AAF57550	Aaf57550 Human cal
10	5911	100.0	5482	6	ABS74268	Abs74268 Human cDN
11	5911	100.0	5482	9	ACD25666	Acd25666 Human cDN
12	5911	100.0	5730	13	ABD32813	Abd32813 Human. can
13	5900.5	99.8	3441	13	ADU20907	Adu20907 Human vol
14	5900.5	99.8	5733	13	ABD32812	Abd32812 Human can
15	5887.5	99.6	3519	13	ADU20909	Adu20909 Human vol
16	5881	99.5	4182	13	ABD32814	Abd32814 Human can
17	5753	97.3	3248	4	AAS01405	Aas01405 Human sec
18	5753	97.3	3248	5	AAF57542	Aaf57542 Human cal
19	5731	97.0	5386	13	ABD32810	Abd32810 Mouse can
20	5704.5	96.5	3588	12	ADO26390	Ado26390 Murine Ca
21	5704	96.5	4993	14	ADY49914	Ady49914 Rat a2d-2
22	5689.5	96.3	5583	12	ADQ23337	Adq23337 Human sof
23	5682.5	96.1	3474	14	ADY49922	Ady49922 Rat a2d-2
24	5641	95.4	3186	4	AAS01404	Aas01404 Human sec
25	5641	95.4	3186	5	AAF57541	Aaf57541 Human cal
26	5533.5	93.6	5279	6	ABS74269	Abs74269 Human cDN
27	5533.5	93.6	5279	9	ACD25667	Acd25667 Human cDN
28	3077.5	52.1	3882	14	ADX26065	Adx26065 Novel cel
29	3050.5	51.6	3965	13	ADR43923	Adr43923 Rat calci
30	3050.5	51.6	3965	14	ADX26192	Adx26192 Novel cel
31	3045	51.5	3802	2	AAT70227	Aat70227 Rabbit ca
32	3045	51.5	3802	2	AAT96812	Aat96812 Rabbit sk
33	3045	51.5	3802	3	AAZ58942	Aaz58942 Rabbit sk
34	3039	51.4	3802	2	AAQ87979	Aaq87979 Rabbit sk
35	3025.5	51.2	3192	4	AAS01422	Aas01422 Pig secre
36	3025.5	51.2	3192	5	AAF57559	Aaf57559 Porcine c
37	3025.5	51.2	3192	14	ADY60713	Ady60713 Truncated
38	3025.5	51.2	3842	4	AAS01419	Aas01419 Pig secre
39	3025.5	51.2	3842	5	AAF57556	Aaf57556 Porcine c
40	3025.5	51.2	3842	14	ADY60710	Ady60710 Calcium c
41	3024	51.2	3579	2	AAQ84669	Aaq84669 Human neu
42	3024	51.2	3579	2	AAV42704	Aav42704 DNA encod
43	3024	51.2	3579	3	AAA71727	Aaa71727 Human cal
44	3024	51.2	3579	6	AAD39979	Aad39979 Human cal
45	3024	51.2	3579	12	ADM57730	Adm57730 Human cal

## ALIGNMENTS

## RESULT 1

AAS01406

ID AAS01406 standard; cDNA; 3327 BP.

XX

AC AAS01406;

XX

DT 04-JUL-2001 (first entry)

XX

DE Human secreted soluble alpha2delta calcium channel subunit #3 cDNA.

XX

KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KW filter binding assay; wheat germ lectin flashplate assay; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3327

FT /\*tag= a

FT /partial

FT /product= "Alpha2delta calcium channel subunit #3"

FT /note= "This sequence lacks a stop codon"

XX

PN WO200119870-A2.

XX

PD 22-MAR-2001.

XX

PF 18-SEP-2000; 2000WO-EP009137.

XX

PR 16-SEP-1999; 99US-00397550.

XX

PA (WARN ) WARNER LAMBERT CO.

XX

PI Brown JP, Bertelli F;

XX

DR WPI; 2001-235262/24.

DR P-PSDB; AAU01016.

XX

PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
PT Wheat Germ Lectin Flashplate assays.

XX

PS Claim 39; Page 57-58; 160pp; English.

XX

CC The present sequence encodes for human secreted calcium channel  
CC alpha2delta subunit #3 which is soluble and retains the functional  
CC characteristics of the full length or wild type alpha2delta subunit  
CC (AAU01025) from which it is derived. The invention relates to truncated  
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
CC which retain their affinity for radioactively labelled gabapentin. The  
CC alpha2delta subunit is 1 of the components of the heteromultimeric  
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal

CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014  
 CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine  
 CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.  
 CC The secreted soluble alpha2delta subunit may be used in assays e.g.  
 CC scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin, L-  
 CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-  
 CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta  
 CC subunit  
 XX  
 SQ Sequence 3327 BP; 770 A; 971 C; 964 G; 622 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3327
Score:	5911.00	Matches:	1109
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-088-876-6 (1-1109) x AAS01406 (1-3327)

Qy	1	MetAlaValProAlaArgThrCysGlyAlaSerArgProGlyProAlaArgThrAlaArg	20
Db	1	ATGGCGGTGCCGGCTCGGACCTGCGGCGCCTCTCGGCCCGGCCAGCGCGGACTGCGCGC	60
Qy	21	ProTrpProGlyCysGlyProHisProGlyProGlyThrArgArgProThrSerGlyPro	40
Db	61	CCCTGGCCCGGCTGCGGCCCCACCCTGGCCCCGGCACCCGGCGCCCGACGTCCGGGCCC	120
Qy	41	ProArgProLeuTrpLeuLeuLeuProLeuLeuProLeuLeuAlaAlaProGlyAlaSer	60
Db	121	CCGCGCCCGCTGTGGCTGCTGCTGCGCTTCTACCGCTGCTCGCCGCCCCGGCGCCTCT	180
Qy	61	AlaTyrSerPheProGlnGlnHisThrMetGlnHisTrpAlaArgArgLeuGluGlnGlu	80
Db	181	GCCTACAGCTTCCCCAGCAGCACACGATGCAGCACTGGGCCCGGCGTCTGGAGCAGGAG	240
Qy	81	ValAspGlyValMetArgIlePheGlyGlyValGlnGlnLeuArgGluIleTyrLysAsp	100
Db	241	GTCGACGGCGTGATGCGGATTTTGGAGGCGTCCAGCAGCTCCGTGAGATTTACAAGGAC	300
Qy	101	AsnArgAsnLeuPheGluValGlnGluAsnGluProGlnLysLeuValGluLysValAla	120
Db	301	AACCGGAACCTGTTTCGAGGTACAGGAGAATGAGCCTCAGAAGTTGGTGGAGAAGGTGGCA	360
Qy	121	GlyAspIleGluSerLeuLeuAspArgLysValGlnAlaLeuLysArgLeuAlaAspAla	140
Db	361	GGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAGGCCCTGAAGAGACTGGCTGATGCT	420
Qy	141	AlaGluAsnPheGlnLysAlaHisArgTrpGlnAspAsnIleLysGluGluAspIleVal	160
Db	421	GCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGACAACATCAAGGAGGAAGACATCGTG	480
Qy	161	TyrTyrAspAlaLysAlaAspAlaGluLeuAspAspProGluSerGluAspValGluArg	180

Db	481	TACTATGACGCCAAGGCTGACGCTGAGCTGGACGACCCTGAGAGTGAGGATGTGGAAAGG	540
Qy	181	GlySerLysAlaSerThrLeuArgLeuAspPheIleGluAspProAsnPheLysAsnLys	200
Db	541	GGGTCTAAGGCCAGCACCTAAGGCTGGACTTCATCGAGGACCCAACTTCAAGAACAAG	600
Qy	201	ValAsnTyrSerTyrAlaAlaValGlnIleProThrAspIleTyrLysGlySerThrVal	220
Db	601	GTCAACTATTTCATACGCGGCTGTACAGATCCCTACGGACATCTACAAAGGCTCCACTGTC	660
Qy	221	IleLeuAsnGluLeuAsnTrpThrGluAlaLeuGluAsnValPheMetGluAsnArgArg	240
Db	661	ATCCTCAATGAGCTCAACTGGACAGAGGCCCTGGAGAATGTGTTTCATGGAAAACCGCAGA	720
Qy	241	GlnAspProThrLeuLeuTrpGlnValPheGlySerAlaThrGlyValThrArgTyrTyr	260
Db	721	CAAGACCCACACTGCTGTGGCAGGTCTTCGGCAGCGCCACAGGAGTCACTCGCTACTAC	780
Qy	261	ProAlaThrProTrpArgAlaProLysLysIleAspLeuTyrAspValArgArgArgPro	280
Db	781	CCGGCCACCCCGTGGCGAGCCCCAAGAAGATCGACCTGTACGATGTCCGAAGGAGACCC	840
Qy	281	TrpTyrIleGlnGlyAlaSerSerProLysAspMetValIleIleValAspValSerGly	300
Db	841	TGGTATATCCAGGGGGCCTCGTCACCCAAAGACATGGTCATCATCGTGGATGTGAGTGGC	900
Qy	301	SerValSerGlyLeuThrLeuLysLeuMetLysThrSerValCysGluMetLeuAspThr	320
Db	901	AGTGTGAGCGGCCTGACCCTGAAGCTGATGAAGACATCTGTCTGCGAGATGCTGGACACG	960
Qy	321	LeuSerAspAspAspTyrValAsnValAlaSerPheAsnGluLysAlaGlnProValSer	340
Db	961	CTGTCTGATGATGACTATGTGAATGTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA	1020
Qy	341	CysPheThrHisLeuValGlnAlaAsnValArgAsnLysLysValPheLysGluAlaVal	360
Db	1021	TGCTTCACACACCTGGTGCAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTG	1080
Qy	361	GlnGlyMetValAlaLysGlyThrThrGlyTyrLysAlaGlyPheGluTyrAlaPheAsp	380
Db	1081	CAGGGCATGGTGGCCAAGGGCACACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGAC	1140
Qy	381	GlnLeuGlnAsnSerAsnIleThrArgAlaAsnCysAsnLysMetIleMetMetPheThr	400
Db	1141	CAGCTGCAGAACTCCAACATCACTCGGGCCAACTGCAACAAGATGATCATGATGTTACAG	1200
Qy	401	AspGlyGlyGluAspArgValGlnAspValPheGluLysTyrAsnTrpProAsnArgThr	420
Db	1201	GATGGTGGTGAGGACCGCTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACG	1260
Qy	421	ValArgValPheThrPheSerValGlyGlnHisAsnTyrAspValThrProLeuGlnTrp	440
Db	1261	GTGCGCGTGTTTACTTTCTCCGTGGGGCAGCATAACTATGACGTACACCGCTGCAGTGG	1320
Qy	441	MetAlaCysAlaAsnLysGlyTyrTyrPheGluIleProSerIleGlyAlaIleArgIle	460